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02-09-01

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/760,285 DATE: 01/29/2001
 TIME: 13:51:01

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3 <110> APPLICANT: Nicolaides, Nicholas C
4   Grasso, Luigi
5   Sass, Philip M
7 <120> TITLE OF INVENTION: CHEMICAL INHIBITORS OF MISMATCH REPAIR
9 <130> FILE REFERENCE: MOR-0017
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/760,285
12 <141> CURRENT FILING DATE: 2001-01-15
14 <160> NUMBER OF SEQ ID NOS: 44
16 <170> SOFTWARE: PatentIn Ver. 2.1
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71 <211> LENGTH: 22

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72 <212> TYPE: DNA
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76 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
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86 <213> ORGANISM: Artificial Sequence
88 <220> FEATURE:
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92 <400> SEQUENCE: 6
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96 <210> SEQ ID NO: 7
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98 <212> TYPE: DNA
99 <213> ORGANISM: Artificial Sequence
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137 <212> TYPE: DNA
138 <213> ORGANISM: Artificial Sequence
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141 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide

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166 <220> FEATURE:
167 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
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177 <213> ORGANISM: Artificial Sequence
179 <220> FEATURE:
180 <223> OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
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188 <211> LENGTH: 859
189 <212> TYPE: PRT
190 <213> ORGANISM: MUS musculus
192 <400> SEQUENCE: 14
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194   1           5           10          15
196 Pro Ile Asp Gly Lys Ser Val His Gln Ile Cys Ser Gly Gln Val Ile
197   20          25          30
199 Leu Ser Leu Ser Thr Ala Val Lys Glu Leu Ile Glu Asn Ser Val Asp
200   35          40          45
202 Ala Gly Ala Thr Thr Ile Asp Leu Arg Leu Lys Asp Tyr Gly Val Asp
203   50          55          60
205 Leu Ile Glu Val Ser Asp Asn Gly Cys Gly Val Glu Glu Asn Phe
206   65          70          75          80
208 Glu Gly Leu Ala Leu Lys His His Thr Ser Lys Ile Gln Glu Phe Ala
209   85          90          95
211 Asp Leu Thr Gln Val Glu Thr Phe Gly Phe Arg Gly Glu Ala Leu Ser
212   100         105         110

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214 Scr Leu Cys Ala Leu Ser Asp Val Thr Ile Ser Thr Cys His Gly Ser
 215 115 120 125
 217 Ala Ser Val Gly Thr Arg Leu Val Phe Asp His Asn Gly Lys Ile Thr
 218 130 135 140
 220 Gln Lys Thr Pro Tyr Pro Arg Pro Lys Gly Thr Thr Val Ser Val Gln
 221 145 150 155 160
 223 His Leu Phe Tyr Thr Leu Pro Val Arg Tyr Lys Glu Phe Gln Arg Asn
 224 165 170 175
 226 Ile Lys Lys Glu Tyr Ser Lys Met Val Gln Val Leu Gln Ala Tyr Cys
 227 180 185 190
 229 Ile Ile Scr Ala Gly Val Arg Val Ser Cys Thr Asn Gln Leu Gly Gln
 230 195 200 205
 232 Gly Lys Arg His Ala Val Val Cys Thr Ser Gly Thr Ser Gly Met Lys
 233 210 215 220
 235 Glu Asn Ile Gly Ser Val Phe Gly Gln Lys Gln Leu Gln Ser Leu Ile
 236 225 230 235 240
 238 Pro Phe Val Gln Leu Pro Pro Ser Asp Ala Val Cys Glu Glu Tyr Gly
 239 245 250 255
 241 Leu Ser Thr Ser Gly Arg His Lys Thr Phe Ser Thr Phe Arg Ala Ser
 242 260 265 270
 244 Phe His Ser Ala Arg Thr Ala Pro Gly Gly Val Gln Gln Thr Gly Ser
 245 275 280 285
 247 Phe Ser Ser Ser Ile Arg Gly Pro Val Thr Gln Gln Arg Ser Leu Ser
 248 290 295 300
 250 Leu Ser Met Arg Phe Tyr His Met Tyr Asn Arg His Gln Tyr Pro Phe
 251 305 310 315 320
 253 Val Val Leu Asn Val Ser Val Asp Ser Gln Cys Val Asp Ile Asn Val
 254 325 330 335
 256 Thr Pro Asp Lys Arg Gln Ile Leu Leu Gln Glu Glu Lys Leu Leu
 257 340 345 350
 259 Ala Val Leu Lys Thr Ser Leu Ile Gly Met Phe Asp Ser Asp Ala Asn
 260 355 360 365
 262 Lys Leu Asn Val Asn Gln Gln Pro Leu Leu Asp Val Glu Gly Asn Leu
 263 370 375 380
 265 Val Lys Leu His Thr Ala Glu Leu Glu Lys Pro Val Pro Gly Lys Gln
 266 385 390 395 400
 268 Asp Asn Ser Pro Ser Leu Lys Ser Thr Ala Asp Glu Lys Arg Val Ala
 269 405 410 415
 271 Ser Ile Ser Arg Leu Arg Glu Ala Phe Ser Leu His Pro Thr Lys Glu
 272 420 425 430
 274 Ile Lys Ser Arg Gly Pro Glu Thr Ala Glu Leu Thr Arg Ser Phe Pro
 275 435 440 445
 277 Ser Glu Lys Arg Gly Val Leu Ser Ser Tyr Pro Ser Asp Val Ile Ser
 278 450 455 460
 280 Tyr Arg Gly Leu Arg Gly Ser Gln Asp Lys Leu Val Ser Pro Thr Asp
 281 465 470 475 480
 283 Ser Pro Gly Asp Cys Met Asp Arg Glu Lys Ile Glu Lys Asp Ser Gly
 284 485 490 495
 286 Leu Ser Ser Thr Ser Ala Gly Ser Glu Glu Phe Ser Thr Pro Glu

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287      500      505      510
289 Val Ala Ser Ser Phe Ser Ser Asp Tyr Asn Val Ser Ser Leu Glu Asp
290      515      520      525
292 Arg Pro Ser Gln Glu Thr Ile Asn Cys Gly Asp Leu Asp Cys Cys Arg Pro
293      530      535      540
295 Pro Gly Thr Gly Gln Ser Leu Lys Pro Glu Asp His Gly Tyr Gln Cys
296 545      550      555      560
298 Lys Ala Leu Pro Leu Ala Arg Leu Ser Pro Thr Asn Ala Lys Arg Phe
299      565      570      575
301 Lys Thr Glu Glu Arg Pro Ser Asn Val Asn Ile Ser Gln Arg Leu Pro
302      580      585      590
304 Gly Pro Gln Ser Thr Ser Ala Ala Glu Val Asp Val Ala Ile Lys Met
305      595      600      605
307 Asn Lys Arg Ile Val Leu Leu Glu Phe Ser Leu Ser Ser Leu Ala Lys
308      610      615      620
310 Arg Met Lys Gln Leu Gln His Leu Lys Ala Gln Asn Lys His Glu Leu
311 625      630      635      640
313 Ser Tyr Arg Lys Phe Arg Ala Lys Ile Cys Pro Gly Glu Asn Gln Ala
314      645      650      655
316 Ala Glu Asp Glu Leu Arg Lys Glu Ile Ser Lys Ser Met Phe Ala Glu
317      660      665      670
319 Met Glu Ile Leu Gly Gln Phe Asn Leu Gly Phe Ile Val Thr Lys Leu
320      675      680      685
322 Lys Glu Asp Leu Phe Leu Val Asp Gln His Ala Ala Asp Glu Lys Tyr
323      690      695      700
325 Asn Phe Glu Met Leu Gln Gln His Thr Val Leu Gln Ala Gln Arg Leu
326 705      710      715      720
328 Ile Thr Pro Gln Thr Leu Asn Leu Thr Ala Val Asn Glu Ala Val Leu
329      725      730      735
331 Ile Glu Asn Leu Glu Ile Phe Arg Lys Asn Gly Phe Asp Phe Val Ile
332      740      745      750
334 Asp Glu Asp Ala Pro Val Thr Glu Arg Ala Lys Leu Ile Ser Leu Pro
335      755      760      765
337 Thr Ser Lys Asn Trp Thr Phe Gly Pro Gln Asp Ile Asp Glu Leu Ile
338      770      775      780
340 Phe Met Leu Ser Asp Ser Pro Gly Val Met Cys Arg Pro Ser Arg Val
341 785      790      795      800
343 Arg Gln Met Phe Ala Ser Arg Ala Cys Arg Lys Ser Val Met Ile Gly
344      805      810      815
346 Thr Ala Leu Asn Ala Ser Glu Met Lys Lys Leu Ile Thr His Met Gly
347      820      825      830
349 Glu Met Asp His Pro Trp Asn Cys Pro His GLy Arg Pro Thr Met Arg
350      835      840      845
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356 <210> SEQ ID NO: 15
357 <211> LENGTH: 3056
358 <212> TYPE: DNA
359 <213> ORGANISM: Mus musculus

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number